

SEQUENCE LISTING

<110> RIKEN

<120> A cell death inducing factor, a cell and an animal expressing the same, and a method for screening an anti cell death treating medicament

<130> RFH14-022N

<140>

<141>

<150> JP 2001/294794

<151> 2001-09-26

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1768

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (29).. (1405)

<400> 1

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Met Ala Ala Pro Arg Ala Gly Arg

1

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ggc gca ggc tgg agc ctt cgg gca tgg cgg gct ttg ggg ggc att cgc 100

Gly Ala Gly Trp Ser Leu Arg Ala Trp Arg Ala Leu Gly Gly Ile Arg

10

15

20

tgg ggg agg aga ccc cgt ttg acc cct gac ctc cgg gcc ctg ctg acg 148

Trp Gly Arg Arg Pro Arg Leu Thr Pro Asp Leu Arg Ala Leu Leu Thr

25

30

35

40

tca gga act tct gac ccc cgg gcc cga gtg act tat ggg acc ccc agt 196

Ser Gly Thr Ser Asp Pro Arg Ala Arg Val Thr Tyr Gly Thr Pro Ser

45

50

55

ctc tgg gcc cgg ttg tct gtt ggg gtc act gaa ccc cga gca tgc ctg 244

Leu Trp Ala Arg Leu Ser Val Gly Val Thr Glu Pro Arg Ala Cys Leu

60

65

70

acg tct ggg acc ccg ggt ccc cgg gca caa ctg act gcg gtg acc cca 292

Thr Ser Gly Thr Pro Gly Pro Arg Ala Gln Leu Thr Ala Val Thr Pro

75

80

85

gat acc agg acc cgg gag gcc tca gag aac tct gga acc cgt tcg cgc 340

Asp Thr Arg Thr Arg Glu Ala Ser Glu Asn Ser Gly Thr Arg Ser Arg

90

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gcg tgg ctg gcg gtg gcg ctg ggc gct ggg ggg gca gtg ctg ttg ttg 388

Ala Trp Leu Ala Val Ala Leu Gly Ala Gly Gly Ala Val Leu Leu Leu

105

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115

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ttg tgg ggc ggg ggt cgg ggt cct ccg gcc gtc ctc gcc gcc gtc cct 436
 Leu Trp Gly Gly Gly Arg Gly Pro Pro Ala Val Leu Ala Ala Val Pro

125

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agc ccg ccg ccc gct tct ccc cgg agt cag tac aac ttc atc gca gat 484
 Ser Pro Pro Pro Ala Ser Pro Arg Ser Gln Tyr Asn Phe Ile Ala Asp

140

145

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gtg gtg gag aag aca gca cct gcc gtg gtc tat atc gag atc ctg gac 532
 Val Val Glu Lys Thr Ala Pro Ala Val Val Tyr Ile Glu Ile Leu Asp

155

160

165

cgg cac cct ttc ttg ggc cgc gag gtc cct atc tcg aac ggc tca gga 580
 Arg His Pro Phe Leu Gly Arg Glu Val Pro Ile Ser Asn Gly Ser Gly

170

175

180

ttc gtg gtg gct gcc gat ggg ctc att gtc acc aac gcc cat gtg gtg 628
 Phe Val Val Ala Ala Asp Gly Leu Ile Val Thr Asn Ala His Val Val

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gct gat cgg cgc aga gtc cgt gtg aga ctg cta agc ggc gac acg tat 676
 Ala Asp Arg Arg Arg Val Arg Val Arg Leu Leu Ser Gly Asp Thr Tyr

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gag gcc gtg gtc aca gct gtg gat ccc gtg gca gac atc gca acg ctg 724
 Glu Ala Val Val Thr Ala Val Asp Pro Val Ala Asp Ile Ala Thr Leu

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agg att cag act aag gag cct ctc ccc acg ctg cct ctg gga cgc tca 772

Arg Ile Gln Thr Lys Glu Pro Leu Pro Thr Leu Pro Leu Gly Arg Ser
 235 240 245

gct gat gtc cgg caa ggg gag ttt gtt gtt gcc atg gga agt ccc ttt 820
 Ala Asp Val Arg Gln Gly Glu Phe Val Val Ala Met Gly Ser Pro Phe
 250 255 260

gca ctg cag aac acg atc aca tcc ggc att gtt agc tct gct cag cgt 868
 Ala Leu Gln Asn Thr Ile Thr Ser Gly Ile Val Ser Ser Ala Gln Arg
 265 270 275 280

cca gcc aga gac ctg gga ctc ccc caa acc aat gtg gaa tac att caa 916
 Pro Ala Arg Asp Leu Gly Leu Pro Gln Thr Asn Val Glu Tyr Ile Gln
 285 290 295

act gat gca gct att gat ttt gga aac tct gga ggt ccc ctg gtt aac 964
 Thr Asp Ala Ala Ile Asp Phe Gly Asn Ser Gly Gly Pro Leu Val Asn
 300 305 310

ctg gat ggg gag gtg att gga gtg aac acc atg aag gtc aca gct gga 1012
 Leu Asp Gly Glu Val Ile Gly Val Asn Thr Met Lys Val Thr Ala Gly
 315 320 325

atc tcc ttt gcc atc cct tct gat cgt ctt cga gag ttt ctg cat cgt 1060
 Ile Ser Phe Ala Ile Pro Ser Asp Arg Leu Arg Glu Phe Leu His Arg
 330 335 340

ggg gaa aag aag aat tcc tcc tcc gga atc agt ggg tcc cag cgg cgc 1108
 Gly Glu Lys Lys Asn Ser Ser Ser Gly Ile Ser Gly Ser Gln Arg Arg
 345 350 355 360

tac att ggg gtg atg atg ctg acc ctg agt ccc agc atc ctt gct gaa 1156
 Tyr Ile Gly Val Met Met Leu Thr Leu Ser Pro Ser Ile Leu Ala Glu

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cta cag ctt cga gaa cca agc ttt ccc gat gtt cag cat ggt gta ctc 1204
 Leu Gln Leu Arg Glu Pro Ser Phe Pro Asp Val Gln His Gly Val Leu

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atc cat aaa gtc atc ctg ggc tcc cct gca cac cgg gct ggt ctg cgg 1252
 Ile His Lys Val Ile Leu Gly Ser Pro Ala His Arg Ala Gly Leu Arg

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cct ggt gat gtg att ttg gcc att ggg gag cag atg gta caa aat gct 1300
 Pro Gly Asp Val Ile Leu Ala Ile Gly Glu Gln Met Val Gln Asn Ala

410

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gaa gat gtt tat gaa gct gtt cga acc caa tcc cag ttg gca gtg cag 1348
 Glu Asp Val Tyr Glu Ala Val Arg Thr Gln Ser Gln Leu Ala Val Gln

425

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435

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atc cgg cgg gga cga gaa aca ctg acc tta tat gtg acc cct gag gtc 1396
 Ile Arg Arg Gly Arg Glu Thr Leu Thr Leu Tyr Val Thr Pro Glu Val

445

450

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aca gaa tga atagatcacc aagagtatga ggctcctgct ctgatttcct 1445
 Thr Glu

ccttgccctt cttgctgagg ttctgagggc accgagacag agggttaaat gaaccagttg 1505

gggcaggicc ctccaaccac cagcaatgac tcctgggctc tgaagaatca cagaaacact 1565

ttttatataa aataaaatta tacctagcaa cataattatag taaaaaatga ggtgggaggg 1625

ctggatcttt tccccacca aaaggctaga ggtaaagctg tatcccccta aacttagggg 1685

agatactgga gctgaccatc ctgacctcct attaaagaaa atgagctgct gccatctttt 1745

gtgggcagtt agtcagggtgc tgc 1768

<210> 2

<211> 458

<212> PRT

<213> Homo sapiens

<400> 2

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Trp Arg Ala Leu Gly Gly Ile Arg Trp Gly Arg Arg Pro Arg Leu Thr

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Pro Asp Leu Arg Ala Leu Leu Thr Ser Gly Thr Ser Asp Pro Arg Ala

35 40 45

Arg Val Thr Tyr Gly Thr Pro Ser Leu Trp Ala Arg Leu Ser Val Gly

50 55 60

Val Thr Glu Pro Arg Ala Cys Leu Thr Ser Gly Thr Pro Gly Pro Arg

65 70 75 80

Ala Gln Leu Thr Ala Val Thr Pro Asp Thr Arg Thr Arg Glu Ala Ser

85 90 95

Glu Asn Ser Gly Thr Arg Ser Arg Ala Trp Leu Ala Val Ala Leu Gly

100	105	110	
Ala Gly Gly Ala Val Leu Leu Leu Leu Trp Gly Gly Gly Arg Gly Pro			
115	120	125	
Pro Ala Val Leu Ala Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg			
130	135	140	
Ser Gln Tyr Asn Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala			
145	150	155	160
Val Val Tyr Ile Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu			
165	170	175	
Val Pro Ile Ser Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu			
180	185	190	
Ile Val Thr Asn Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val			
195	200	205	
Arg Leu Leu Ser Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp			
210	215	220	
Pro Val Ala Asp Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu			
225	230	235	240
Pro Thr Leu Pro Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe			
245	250	255	
Val Val Ala Met Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser			
260	265	270	
Gly Ile Val Ser Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro			
275	280	285	
Gln Thr Asn Val Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly			
290	295	300	
Asn Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val			
305	310	315	320
Asn Thr Met Lys Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp			
325	330	335	
Arg Leu Arg Glu Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser			

340 345 350
 Gly Ile Ser Gly Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr
 355 360 365
 Leu Ser Pro Ser Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe
 370 375 380
 Pro Asp Val Gln His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser
 385 390 395 400
 Pro Ala His Arg Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile
 405 410 415
 Gly Glu Gln Met Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg
 420 425 430
 Thr Gln Ser Gln Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu
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 Thr Leu Tyr Val Thr Pro Glu Val Thr Glu
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Synthetic

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<210> 4

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic

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